

# SEQUENCE LISTING

<110> APPLICANT: Geiser, Martin  
 Geisse, Sabine  
 Ostermeier, Christian  
 Ramage, Paul  
 Raulf, Friedrich  
 Zenke, Gerhard

<120> TITLE: ATOMIC STRUCTURE OF THE CATALYTIC DOMAIN  
 FOR USE IN DESIGNING AND IDENTIFYING INHIBITORS OF ZAP-70  
 KINASE

<130> DOCKET/FILE REFERENCE: 4-32688A

<140> CURRENT APPLICATION NUMBER: US10/528,709

<141> FILING DATE: 2003-09-25

<150> PRIOR APPLICATION NUMBER: PCT/EP03/10686

<151> FILING DATE: 2003-09-25

<150> PRIOR APPLICATION NUMBER: 60/413,704

<151> FILING DATE: 2002-09-26

<160> NUMBER OF SEQUENCES: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO:1

<211> LENGTH: 619

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQ ID NO:1

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			20					25					30		
Leu	Phe	Leu	Leu	Arg	Gln	Cys	Leu	Arg	Ser	Leu	Gly	Gly	Tyr	Val	Leu
		35					40					45			
Ser	Leu	Val	His	Asp	Val	Arg	Phe	His	His	Phe	Pro	Ile	Glu	Arg	Gln
	50					55					60				
Leu	Asn	Gly	Thr	Tyr	Ala	Ile	Ala	Gly	Gly	Lys	Ala	His	Cys	Gly	Pro
65					70				75						80
Ala	Glu	Leu	Cys	Glu	Phe	Tyr	Ser	Arg	Asp	Pro	Asp	Gly	Leu	Pro	Cys
				85					90					95	
Asn	Leu	Arg	Lys	Pro	Cys	Asn	Arg	Pro	Ser	Gly	Leu	Glu	Pro	Gln	Pro
			100					105					110		
Gly	Val	Phe	Asp	Cys	Leu	Arg	Asp	Ala	Met	Val	Arg	Asp	Tyr	Val	Arg
		115					120					125			
Gln	Thr	Trp	Lys	Leu	Glu	Gly	Glu	Ala	Leu	Glu	Gln	Ala	Ile	Ile	Ser
	130					135					140				
Gln	Ala	Pro	Gln	Val	Glu	Lys	Leu	Ile	Ala	Thr	Thr	Ala	His	Glu	Arg
145					150					155					160
Met	Pro	Trp	Tyr	His	Ser	Ser	Leu	Thr	Arg	Glu	Glu	Ala	Glu	Arg	Lys

				165					170					175	
Leu	Tyr	Ser	Gly	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg
			180					185					190		
Lys	Glu	Gln	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val
		195					200					205			
Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro
	210				215						220				
Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys
225				230					235						240
Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn
			245					250						255	
Ser	Ser	Ala	Ser	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala
		260					265						270		
His	Pro	Ser	Thr	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn
		275					280					285			
Ser	Asp	Gly	Tyr	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys
	290				295						300				
Pro	Arg	Pro	Met	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser
305				310						315					320
Asp	Pro	Glu	Glu	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn
			325					330						335	
Leu	Leu	Ile	Ala	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val
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Arg	Gln	Gly	Val	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile
	355						360					365			
Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met	Met
	370				375						380				
Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val	Arg
385				390						395					400
Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu	Met
			405					410						415	
Ala	Gly	Gly	Gly	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu	Glu
		420						425					430		
Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly
	435					440					445				
Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala
	450				455						460				
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465				470						475					480
Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg
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<210> SEQ ID NO:2  
 <211> LENGTH: 322  
 <212> TYPE: PRT  
 <213> ORGANISM:Homo sapiens

<400> SEQ ID NO:2  
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 1 5 10 15  
 Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys  
 20 25 30  
 Leu Phe Leu Lys Arg Asp Asn Leu Ile Ala Asp Ile Glu Leu Gly  
 35 40 45  
 Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys  
 50 55 60  
 Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys  
 65 70 75 80  
 Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu  
 85 90 95  
 Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala  
 100 105 110  
 Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu His Lys Phe  
 115 120 125  
 Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu  
 130 135 140  
 Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe  
 145 150 155 160  
 Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His  
 165 170 175  
 Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp  
 180 185 190  
 Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp  
 195 200 205  
 Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp  
 210 215 220  
 Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln  
 225 230 235 240  
 Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu  
 245 250 255  
 Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr  
 260 265 270  
 Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp  
 275 280 285  
 Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala  
 290 295 300  
 Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala  
 305 310 315 320  
 Cys Ala

<210> SEQ ID NO:3  
 <211> LENGTH: 74  
 <212> TYPE: DNA  
 <213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG474

<400> SEQ ID NO:3  
cagatggata cacccttgag ccagcactgg aagttctgtt ccagggggccc cgcataacgt 60  
ccccagacaa accg 74

<210> SEQ ID NO:4  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide RS366

<400> SEQ ID NO:4  
acaacgcaca gaatctagcg 20

<210> SEQ ID NO:5  
<211> LENGTH: 74  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG475

<400> SEQ ID NO:5  
cacactccca gccaccccat ccacgctgga agttctgttc cagggggccct tgactcatcc 60  
tcagagacga atcg 74

<210> SEQ ID NO:6  
<211> LENGTH: 57  
<212> TYPE: DNA  
<213> ORGANISM:Unknown

<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide MG479

<400> SEQ ID NO:6  
gctcgaattc tcaatgatga tgatgatgat gggcacaggc agcctcagcc ttctgtg 57